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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/987,755

DATE: 11/20/2001

TIME: 09:47:58

Input Set : A:\198D1C1.ST25.txt

Output Set: N:\CRF3\11202001\I987755.raw

ENTERED

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3 <110> APPLICANT: Kunsch et al
5 <120> TITLE OF INVENTION: Human Hepatoma-Derived Growth Factor-2
7 <130> FILE REFERENCE: PF198D1C1
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/987,755
10 <141> CURRENT FILING DATE: 2001-11-15
12 <150> PRIOR APPLICATION NUMBER: 09/263,625
13 <151> PRIOR FILING DATE: 1999-03-05
15 <150> PRIOR APPLICATION NUMBER: 08/464,600
16 <151> PRIOR FILING DATE: 1995-06-05
18 <160> NUMBER OF SEQ ID NOS: 7
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3202
24 <212> TYPE: DNA
25 <213> ORGANISM: human
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (34)..(780)
30 <223> OTHER INFORMATION:
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35                                     Met Ala Ala Val Ser Leu Arg
36                                     1           5
38 ctc ggc gac ttg gtg tgg ggg aaa ctc ggc cga tat cct cct tgg cca      102
39 Leu Gly Asp Leu Val Trp Gly Lys Leu Gly Arg Tyr Pro Pro Trp Pro
40      10           15           20
42 gga aag att gtt aat cca cca aag gac ttg aag aaa cct cgc gga aag      150
43 Gly Lys Ile Val Asn Pro Pro Lys Asp Leu Lys Lys Pro Arg Gly Lys
44      25           30           35
46 aaa tgc ttc ttt gtg aaa ttt ttt gga aca gaa gat cat gcc tgg atc      198
47 Lys Cys Phe Phe Val Lys Phe Phe Gly Thr Glu Asp His Ala Trp Ile
48 40           45           50           55
50 aaa gtg gaa cag ctg aag cca tat cat gct cat aaa gag gaa atg ata      246
51 Lys Val Glu Gln Leu Lys Pro Tyr His Ala His Lys Glu Glu Met Ile
52      60           65           70
54 aaa att aac aag ggt aaa cga ttc cag caa gcg gta gat gct gtc gaa      294
55 Lys Ile Asn Lys Gly Lys Arg Phe Gln Gln Ala Val Asp Ala Val Glu
56      75           80           85
58 gag ttc ctc agg aga gcc aaa ggg aaa gac cag acg tca tcc cac aat      342
59 Glu Phe Leu Arg Arg Ala Lys Gly Lys Asp Gln Thr Ser Ser His Asn
60      90           95          100
62 tct tct gat gac aag aat cga cgt aat tcc agt gag gag aga agt agg      390
63 Ser Ser Asp Asp Lys Asn Arg Arg Asn Ser Ser Glu Glu Arg Ser Arg
64      105          110          115
66 cca aac tca ggt gat gag aag cgc aaa ctt agc ctg tct gaa ggg aag      438
67 Pro Asn Ser Gly Asp Glu Lys Arg Lys Leu Ser Leu Ser Glu Gly Lys
68 120          125          130          135

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70 gtg aag aag aac atg gga gaa gga aag aag agg gtg tct tca ggc tct      486
71 Val Lys Lys Asn Met Gly Glu Gly Lys Lys Arg Val Ser Ser Gly Ser
72              140              145              150
74 tca gag aga ggc tcc aaa tcc cct ctg aaa aga gcc caa gag caa agt      534
75 Ser Glu Arg Gly Ser Lys Ser Pro Leu Lys Arg Ala Gln Glu Gln Ser
76              155              160              165
78 ccc cgg aag cgg ggt cgg ccc cca aag gat gag aag gat ctc acc atc      582
79 Pro Arg Lys Arg Gly Arg Pro Pro Lys Asp Glu Lys Asp Leu Thr Ile
80              170              175              180
82 ccg gag tct agt acc gtg aag ggg atg atg gcc gga ccg atg gcc gcg      630
83 Pro Glu Ser Ser Thr Val Lys Gly Met Met Ala Gly Pro Met Ala Ala
84              185              190              195
86 ttt aaa tgg cag cca acc gca agc gag cct gtt aaa gat gca gat cct      678
87 Phe Lys Trp Gln Pro Thr Ala Ser Glu Pro Val Lys Asp Ala Asp Pro
88 200              205              210              215
90 cat ttc cat cat ttc ctg cta agc caa aca gag aag cca gct gtc tgt      726
91 His Phe His His Phe Leu Leu Ser Gln Thr Glu Lys Pro Ala Val Cys
92              220              225              230
94 tac cag gca atc acg aag aag ttg aaa ata tgt gaa gac ctc ctt ctt      774
95 Tyr Gln Ala Ile Thr Lys Lys Leu Lys Ile Cys Glu Asp Leu Leu Leu
96              235              240              245
98 cct agg tgaagtggc aatgcagcca agatgatgct gatcgtgaac atggtccaag      830
99 Pro Arg
102 ggagcttcat ggccactatt gccgaggggc tgaccctggc ccaggtgaca ggccagtccc      890
104 agcagacact cttggacatc ctcaatcagg gacagttggc cagcatcttc ctggaccaga      950
106 agtgccaaaa tatcctgcaa ggaaacttta agcctgattt ctacctgaaa tacattcaga      1010
108 aggatctccg cttagccatt gcgctgggtg atgcggtcaa ccaccgact cccatggcag      1070
110 ctgcagcaaa tgaggtgtac aaaagagcca aggcgctgga ccagtctgac aacgatatgt      1130
112 ccgccgtgta ccgagcctac atacactaag ctgtcgacac ccgccctca cccctccaat      1190
114 ccccccctctg acccccctctt cctcacatgg ggtcgggggc ctgggagttc attctggtac      1250
116 cagcccacct atctccattt ccttttatac agactttgag acttgccatc agcacagcac      1310
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128 agaggctgta gtcattgtccc catccccac tggattccct acaaggagag gccttgggcc      1670
130 cagatgagcc agtacagact ccagacagag gggcccttgg ggccctccaa cctcaggtga      1730
132 tgagctgaga aagatgttca cgtctaagcg tccagtgtgc acccagcgct ccatagacgc      1790
134 ctttgtgaac tgaaaagaga ctggcagagt cccgagaaga tggggccctg gctttccagg      1850
136 gagtgcagca agcagccggc ctgcaggtga gcatggaggc ccggccctca ccgcctcgaa      1910
138 gccatgcccc agatgccact gccacagcgg gcgctcgctc ctccctaggc tgttttagta      1970
140 tttggatttg cattccatcc cttgggaggg agtccctcagg gccactagtg atgagccaag      2030
142 aggagtgggg gttggggggc ctcccttctg ttcccgttag gccacagact cttcacctgg      2090
144 ctctgactta cctcggtccc ctcccagtg tcccaccttc tccacctgc cctgccaaat      2150
146 cccctgcatg cccaccgctc tccatcctcc ctccctctcc tcttccctcc gtggagacag      2210
148 tatttctttc tgtctgtccc tttggcccag acccagcctg accaacgatg agcatttctt      2270
150 aggctcagct cttgatacgg aaacgagtggt cttcaactcca gccagcatca tggctctcgg      2330
152 tgcttcccgg gcccgggggtc tgtcgggagg gaagagaact gggcctgacc tacctgaact      2390

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154 gactggccct ccgagggtggg tctgggacat cctagaggcc ctacatttgt ccttgatag 2450
156 gggaccgggg ggggcttggg atgttscaaa aaaaaaagtt acccaaggga tgcagtttt 2510
158 ttatccctct gcatgggttg gattttccaa aatcataatt tgcagaagga aggccagcat 2570
160 ttacgatgca atatgtaatt atatataggg tggccacact agggcggggt ccttcccccc 2630
162 tcacagcttt gggccctttc agagattaga aactgggtta gaggattgca gaagacgagt 2690
164 ggggggaggg cagggaagat gcctgtcggg tttttagcac agttcatttc actgggattt 2750
166 tgaagcattt ctgtctgaac acaaagcctg ttctagtccct ggcggaacac actgggggtg 2810
168 gggcgggggg aagatgcggg aatgaaaccg gttagtcaat tttgtcttaa tattgttgac 2870
170 aattctgtaa agttcctttt tatgaatatt tctgtttaag ctatttcacc tttcttttga 2930
172 aatccttccc ttttaaggag aaaatgtgac actttgtgaa aaagcttgta agaaagcccc 2990
174 tccctttttt ctttaaacct ttaaattgaca aatctaggta attaaggttg tgaattttta 3050
176 tttttgcttt gtttttaatg aacatttgtc tttcagaata ggattgtgtg ataattgtta 3110
178 aatggsaaaa acaaaacatg attttgtgca attaacaag ctactgcaag gaaaataaaa 3170
180 cacttcttgg taacaaaaaa aaaaaaaaaa aa 3202
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 249
185 <212> TYPE: PRT
186 <213> ORGANISM: human
188 <400> SEQUENCE: 2
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191 1 5 10 15
194 Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp
195 20 25 30
198 Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly
199 35 40 45
202 Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His
203 50 55 60
206 Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln
207 65 70 75 80
210 Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys
211 85 90 95
214 Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn
215 100 105 110
218 Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys
219 115 120 125
222 Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys
223 130 135 140
226 Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu
227 145 150 155 160
230 Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys
231 165 170 175
234 Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met
235 180 185 190
238 Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu
239 195 200 205
242 Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln
243 210 215 220
246 Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys
247 225 230 235 240

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250 Ile Cys Glu Asp Leu Leu Leu Pro Arg
251                               245
254 <210> SEQ ID NO: 3
255 <211> LENGTH: 34
256 <212> TYPE: DNA
257 <213> ORGANISM: human
259 <400> SEQUENCE: 3
260 acgtggatcc gcggctgtga gtctgcggct cggc           34
263 <210> SEQ ID NO: 4
264 <211> LENGTH: 35
265 <212> TYPE: DNA
266 <213> ORGANISM: human
268 <400> SEQUENCE: 4
269 caacaagctt tcacctagga agaaggaggt ctcca           35
272 <210> SEQ ID NO: 5
273 <211> LENGTH: 41
274 <212> TYPE: DNA
275 <213> ORGANISM: human
277 <400> SEQUENCE: 5
278 acgaggatcc gccatcatgg cggctgtgag tctgcggctc g           41
281 <210> SEQ ID NO: 6
282 <211> LENGTH: 36
283 <212> TYPE: DNA
284 <213> ORGANISM: human
286 <400> SEQUENCE: 6
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291 <211> LENGTH: 240
292 <212> TYPE: PRT
293 <213> ORGANISM: human
295 <400> SEQUENCE: 7
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298 1                               5                               10                               15
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302                               20                               25                               30
305 Met Pro Glu Ala Ala Val Lys Ser Thr Ala Asn Lys Tyr Gln Val Phe
306                               35                               40                               45
309 Phe Phe Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe
310                               50                               55                               60
313 Pro Tyr Glu Glu Ser Lys Glu Lys Phe Gly Lys Pro Asn Lys Arg Lys
314 65                               70                               75                               80
317 Gly Phe Ser Glu Gly Leu Trp Glu Ile Glu Asn Asn Pro Thr Val Lys
318                               85                               90                               95
321 Ala Ser Gly Tyr Gln Ser Ser Gln Lys Lys Ser Cys Val Glu Glu Pro
322                               100                              105                              110
325 Glu Pro Glu Pro Glu Ala Ala Glu Gly Asp Gly Asp Lys Lys Gly Asn
326                               115                              120                              125
329 Ala Glu Gly Ser Ser Asp Glu Gly Lys Leu Val Ile Asp Glu Pro
330                               130                              135                              140

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333 Ala Lys Glu Lys Asn Glu Lys Gly Ala Leu Lys Arg Arg Ala Gly Asp
334 145                      150                      155                      160
337 Leu Leu Glu Asp Ser Pro Lys Arg Pro Lys Glu Ala Glu Asn Pro Glu
338                      165                      170                      175
341 Gly Glu Glu Lys Glu Ala Ala Thr Leu Glu Val Glu Arg Pro Leu Pro
342                      180                      185                      190
345 Met Glu Val Glu Lys Asn Ser Thr Pro Ser Glu Pro Gly Ser Gly Arg
346                      195                      200                      205
349 Gly Pro Pro Gln Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Ala
350                      210                      215                      220
353 Thr Lys Glu Asp Ala Glu Ala Pro Gly Ile Arg Asp His Glu Ser Leu
354 225                      230                      235                      240

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/987,755

DATE: 11/20/2001

TIME: 09:47:59

Input Set : A:\198D1C1.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number